What is claimed is:

1.   A method of identifying an unknown bioagent using a database of molecular masses of known bioagents comprising:

contacting nucleic acid from said bioagent with at least one pair of oligonucleotide primers that hybridize to sequences of said nucleic acid, wherein said sequences flank a variable nucleic acid sequence of said bioagent;

producing an amplification product of said variable nucleic acid sequence;

determining a first molecular mass of said amplification product; and

comparing said first molecular mass to the molecular masses of known bioagents, thereby identifying the unknown bioagent.

2.   The method of claim 1 wherein said sequences to which said at least one pair of oligonucleotide primers hybridize are highly conserved.

3.   The method of claim 1 wherein said sequences to which said at least one pair of oligonucleotide primers hybridize are highly conserved across at least two species.

4.   The method of claim 1 further comprising the step of isolating a nucleic acid from said bioagent prior to contacting said nucleic acid with said at least one pair of oligonucleotide primers, wherein the comparing step further comprises comparing a base-pair count resulting from a translation of the corresponding molecular mass, and wherein a master database of molecular masses of known bioagents further includes a translation of said molecular masses of known bioagents to corresponding base-pair counts of each known bioagent resulting from a specific primer pair set and comparing the base-pair count of said unknown bioagent against the obtained base-pair count of known bioagents for the selected primer pair set for determining the identity of said unknown bioagent.

5.   The method of claim 4 further comprising the step of reconciling the database of molecular masses of known bioagents with the master database of molecular masses of known bioagents.

6.   The method of claim 1 wherein said bioagent is a bacterium, virus, cell or spore.

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7.   The method of claim 1 wherein said amplification product is ionized by electorospray ionization, matrix assisted laser desorption or fast atom bombardment prior to molecular mass determination.

8.   The method of claim 1 wherein said molecular mass is determined by mass spectrometry.

9.   The method of claim 5 wherein said master database of molecular masses of known bioagents and the database of molecular masses of known bioagents are reconciled over a network.

10.   The method of claim 4 wherein the identity is determined by statistically correlating the molecular mass of the unknown bioagent with at least one molecular mass of said master database.

11.   A database having cell-data positional significance comprising at least a first table of a plurality of data-containing cells, said first table organized into at least a first row and a second row, each row having columns and data-containing cells; and wherein said data-containing cells have an alignment with at least one other row for differentiating aligned from non-aligned data-containing cells, and wherein said differentiation in alignment of said data-containing cells designates a structural feature of a polymer.

12.   The database according to claim 11 wherein said alignment is a vertical alignment according to base pair homology along a linear segment within each polymer.

13.   The database according to claim 11 wherein said vertical alignment further aligns cell-data according to inter-species conserved regions.

14.   The database according to claim 11 wherein the structural feature is a bulge or a loop.

15.   The database according to claim 11 wherein the polymer is an RNA.

16.   A method for reconciling a first file and a second file, said second file corresponding at least in part to said first file, said first file and said second file each containing records, said records corresponding to rows in a table of a dimensional database having rows and columns defined by data-cells having data-cell positional significance, said method comprising:

5   comparing said first file and said corresponding second file with a backup file containing records from a previous reconciliation of said first file and said corresponding second file to identify new, updated or deleted records;

creating a reconcile file containing information pertaining to said new, updated or deleted records identified in said comparing step; and

10   copying the contents of said reconcile file to said first file, said corresponding second file and a new backup file.

17.   A service providing information related to a bioagent comprising:

providing a dimensional master database for storing a molecular mass, an identity and a 15 detail corresponding to a plurality of known bioagents and, said master database storing the molecular mass, the identity and the detail for a plurality of known bioagents;

interrogating the master database with an identification request of an unknown bioagent to generate a response; and

delivering said response from the master database to a requester.

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18.   The service according to claim 17 wherein the molecular mass is of a selected portion of the known bioagent, the identity comprises at least a geographic origin and a name for the known bioagent, and the detail comprises at least a treatment.

25 19.   The service according to claim 17 wherein the request comprises a symptomatology and the identification comprises a recommended pair of primers for hybridizing to sequences of nucleic acid flanking a variable nucleic acid sequence of the unknown bioagent, and said pair of primers are hybridized to the sequences of nucleic acid flanking a variable nucleic acid sequence of the unknown bioagent.

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20.   The service according to claim 19 wherein the nucleic acid sequence of the unknown bioagent between said pair of primers defines the selected portion of both the known bioagents and the unknown bioagent.

21.   The service according to claim 20 wherein the response is delivered through a network.

22.   The service according to claim 20 wherein the request comprises a molecular mass of the unknown bioagent for the selected portion and where the response generated thereto comprises a set of molecular masses for analogous selected portions of know bioagents, and said set comprising at least one molecular mass from the master database.

23.   The service according to claim 21 wherein the network is a local area network.

24.   The service according to claim 21 wherein the network is a wide area network.

25.   The service according to claim 22 wherein the network is the internet.

26.   A method of determining a geographical origin of a selected bioagent using a database of molecular masses of known bioagents comprising:

        contacting nucleic acid from said selected bioagent with at least one pair of oligonucleotide primers which hybridize to sequences of said nucleic acid, wherein said sequences flank a variable nucleic acid sequence of the bioagent;

        producing an amplification product of said variable nucleic acid sequence;

        determining a first molecular mass of said amplification product; and

        comparing said first molecular mass to the molecular masses of known bioagents for determining a geographic origin of said selected bioagent, said comparison determining an identity and a geographic origin of said selected bioagent.

27.   The method of claim 26 wherein said sequences to which said at least one pair of oligonucleotide primers hybridize are highly conserved.

28.   The method of claim 26 wherein said sequences to which said at least one pair of oligonucleotide primers hybridize are highly conserved across species.

29.   The method of claim 26 further comprising the step of isolating a nucleic acid from said selected bioagent prior to contacting said nucleic acid with said at least one pair of oligonucleotide primers, wherein the comparing step further comprises interrogating a master

database of molecular masses of known bioagents for obtaining molecular masses of known bioagents and comparing the molecular mass of said selected bioagent against the obtained molecular masses of known bioagents thereby determining an origin of said selected bioagent.

30.   The method of claim 29 further comprising the step of reconciling the database of molecular masses of known bioagents with the master database of molecular masses of known bioagents.

31.   The method of claim 26 wherein said bioagent is a bacterium, virus, cell or spore.

32.   The method of claim 26 wherein said amplification product is ionized by electorospray ionization, matrix assisted laser desorption or fast atom bombardment prior to molecular mass determination.

33.   The method of claim 26 wherein said molecular mass is determined by mass spectrometry.

34.   The method of claim 29 wherein said master database of molecular masses of known bioagents and the database of molecular masses of known bioagents are reconciled over a network.

35.   The method of claim 29 wherein the origin comprises a statistical group of matching molecular masses and the geographic origin corresponding thereto.